

M.RAO

Re-RUN



1600

## RAW SEQUENCE LISTING

DATE: 03/12/2003

PATENT APPLICATION: US/09/576,778B

TIME: 10:42:33

Input Set : N:\vernette\US09576778B.raw

Output Set: N:\CRF4\03122003\I576778B.raw

1 <110> APPLICANT: Schulein, Martin  
 2 <120> TITLE OF INVENTION: Family 9 Endo-Beta-1, 4-Glucanases  
 3 <130> FILING REFERENCE: 1843.200-US

C--&gt; 5 &lt;140&gt; CURRENT APPLICATION NUMBER: US/09/576,778B

C--&gt; 6 &lt;141&gt; CURRENT FILING DATE: 2000-05-24

7 &lt;160&gt; NUMBER OF SEQ ID NOS: 10

8 &lt;170&gt; SOFTWARE: PatentIn version 3.1

9 &lt;210&gt; SEQ ID NO: 1

10 &lt;211&gt; LENGTH: 1941

11 &lt;212&gt; TYPE: DNA

12 &lt;213&gt; ORGANISM: Bacillus licheniformis

13 &lt;214&gt; FEATURE:

14 &lt;215&gt; NAME/KEY: CDS

15 &lt;216&gt; LOCATION: (1)..(1938)

16 &lt;217&gt; OTHER INFORMATION:

17 &lt;218&gt; FEATURE:

18 &lt;219&gt; NAME/KEY: sig\_peptide

19 &lt;220&gt; LOCATION: (1)..(27)

20 &lt;221&gt; OTHER INFORMATION:

W--&gt; 22 &lt;220&gt;

21 &lt;221&gt; NAME/KEY: mat\_peptide

22 &lt;222&gt; LOCATION: (48)..

23 &lt;223&gt; OTHER INFORMATION:

W--&gt; 26 &lt;400&gt; 1

27	atg aaa gag ctt tgt ttg gow ctt tta gtg atc ttc tct atg agc ata	48
28	Met Lys Ala Leu Cys Leu Ala Leu Leu Val Ile Phe Ser Met Ser Ile	
29	-05 -20 -15	
30	gag tgg ttt tca gaa aag acc cgt gca gct tct gct gaa gaa tat cct	96
31	Ala Ser Phe Ser Glu Lys Thr Arg Ala Ala Ser Ala Glu Glu Tyr Pro	
32	-10 -5 -1 1	
33	asn aat tat gct gaa ctg ctg caa aag tct ttg tta ttt tat gaa gca	144
34	His Asn Tyr Ala Glu Leu Leu Gln Lys Ser Leu Leu Phe Tyr Glu Ala	
35	5 10 15	
36	gag cgc tgg gga aga ctt ccg gaa aac agc cgg ctg aat tgg aga gga	192
37	Gln Arg Ser Gly Arg Leu Pro Glu Asn Ser Arg Leu Asn Trp Arg Gly	
38	20 25 30 35	
39	gac tcc ggg ctt gag gac gga aaa gac gtt ggc ctc gat tta acg gga	240
40	Asp Ser Gly Leu Glu Asp Gly Lys Asp Val Gly Leu Asp Leu Thr Gly	
41	40 45 50	
42	ggg tgg tat gat gcc ggc gac caa gtc aag ttc ggt ctg ccg atg gct	288
43	Gly Trp Tyr Asp Ala Gly Asp His Val Lys Phe Gly Leu Pro Met Ala	
44	55 60 65	

ENTERED

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/576,778B

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15	tat tct gcc gca atc ctg tca tgg tgg gtc tat gag tac cga gat gcc	336
16	Tyr Ser Ala Ala Ile Leu Ser Trp Ser Val Tyr Glu Tyr Arg Asp Ala	
47	75 75 80	
48	tac aaa gaa tgg ggt cag ctt gat ggg ggg cgg gac aat att aat tgg	384
49	Tyr Lys Glu Ser Gly Gln Leu Asp Ala Ala Leu Asp Asn Ile Lys Trp	
50	85 90 95	
51	gat aca gac tac ttt ctt aaa gcc cat aag gct cct tat gaa ttc tgg	432
52	Ala Thr Asp Tyr Phe Leu Lys Ala His Thr Ala Pro Tyr Glu Leu Trp	
53	100 105 110 115	
54	gat cca gtc gga aat ggc gct cta gac caa gaa tgg tgg ggg cca gcc	480
55	Gly Gln Val Gly Asn Gly Ala Leu Asp His Ala Trp Trp Gly Pro Ala	
56	120 125 130	
57	gat gaa atg cgg atg aag cgc cct gcc tat aag atc gat gcc ggt tgt	528
58	Ser Val Met Pro Met Lys Arg Pro Ala Tyr Lys Ile Asp Ala Gly Cys	
59	135 140 145	
60	caa ggg tca gac ctt gct ggt gat aca gcc gaa gcc cta gaa tca gaa	576
61	Pro Gly Ser Asp Leu Ala Gly Gly Thr Ala Ala Ala Leu Ala Ser Ala	
62	150 155 160	
63	tca aat att ttc aag cgg aac gat tat tct tac tct gaa aaa ttc ctg	624
64	Ser Ile Ile Phe Lys Pro Thr Asp Ser Ser Tyr Ser Glu Lys Leu Leu	
65	165 170 175	
66	gct cat gcc aag caa ttg tat gat ttt gcc gac cgc tac cgc ggt aaa	672
67	Ala His Ala Lys Gln Leu Tyr Asp Phe Ala Asp Arg Tyr Arg Gly Lys	
68	180 185 190 195	
69	tat tca gac tgc att aca gcc gaa cag caa tat tat aat tgg tga agc	720
70	Tyr Ser Asp Cys Ile Thr Asp Ala Gln Gln Tyr Tyr Asn Ser Trp Ser	
71	200 205 210	
72	gga tat aca gat gaa ctg aca tgg gga gct gtc tgg ctc tac ttc gaa	768
73	Gly Tyr Lys Asp Glu Leu Thr Trp Gly Ala Val Trp Leu Tyr Leu Ala	
74	215 220 225	
75	aaa gaa gaa caa caa tat ttg gat aaa gcc ctt gct tgg gtc tca gat	816
76	Thr Glu Gln Gln Gln Tyr Leu Asp Lys Ala Leu Ala Ser Val Ser Asp	
77	230 235 240	
78	tgg gcc gat ccc gaa aac tgg cct tac cgc tgg aag ctc tcc tga gat	864
79	Trp Gly Asp Pro Ala Asn Trp Pro Tyr Arg Trp Thr Leu Ser Trp Asp	
80	245 250 255	
81	gat gtc aat tac gga gaa cag ctg ctg ctc gct cgt cgg aca aat gat	912
82	Asp Val Thr Tyr Gly Ala Gln Leu Leu Leu Ala Arg Leu Thr Asn Asp	
83	260 265 270 275	
84	caa cgt ttt gtc aaa tct gtc gaa cgc aat ctt gat tat tgg tca aca	960
85	Ser Arg Phe Val Lys Ser Val Glu Arg Asn Leu Asp Tyr Trp Ser Thr	
86	280 285 290	
87	ggt tac agt cat aat gga agc ata gaa cgg atc aag tat aag ccc gcc	1008
88	Gly Tyr Ser His Asn Gly Ser Ile Glu Arg Ile Thr Tyr Thr Pro Gly	
89	295 300 305	
90	ggg ttg gcc tgg ctt gag cag tgg gga tca ttg cga tac gct tgg aat	1056
91	Gly Leu Ala Trp Leu Glu Gln Trp Gly Ser Leu Arg Tyr Ala Ser Asn	
92	310 315 320	
93	gcc gct ttt ctc gct ttc gtt tat tcc gat tgg gtg gat aca gaa aaa	1104

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Input Set : N:\vernette\US09576778B.raw

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94	Ala Ala Phe Leu Ala Phe Val Tyr Ser Asp Trp Val Asp Thr Glu Lys	
95	325	335
96	ggc aia aga tat cgg gat ttt gct gtt cgg caa acg gac tat atg cta	1152
97	Ala Lys Arg Tyr Arg Asp Phe Ala Val Arg Gln Thr Glu Tyr Met Leu	
98	340	345
99	gga gat aat cgg cag cag cga agc ttt gtc gtt gga tac ggt aaa aat	1200
100	Gly Asp Asn Pro Gln Gln Arg Ser Phe Val Val Gly Tyr Gly Lys Asn	
101	360	365
102	cgg cgg aaa cat cgg cat cgc cgt aca gaa cgc ggt tca tgg gcc aat	1248
103	Pro Pro Lys His Pro His His Arg Thr Ala His Gly Ser Trp Ala Asn	
104	375	380
105	cag atc aat ctg cct gaa aac cat cgg cat acc cta tgc ggc gaa ata	1296
106	Gln Met Asn Val Pro Glu Asn His Arg His Thr Leu Tyr Gly Ala Leu	
107	390	395
108	gtc ggt ggt cgg gga agc gac cat tgg tac cga gat gac ata aca gat	1344
109	Val Gly Gly Pro Gly Arg Asp Asp Ser Tyr Arg Asp Asp Ile Thr Asp	
110	405	410
111	tat cgg tca aac gaa gtt cgg atc gat tat aat gct gct ttt aac ggc	1392
112	Tyr Ala Ser Asn Glu Val Ala Ile Asp Tyr Asn Ala Ala Phe Thr Gly	
113	420	425
114	aac tta ggc aaa atg ttt cag ctg ttc ggc aaa ggc cat gtt cgg ctg	1440
115	Asn Val Ala Lys Met Phe Gln Leu Phe Gly Lys Gly His Val Pro Leu	
116	440	445
117	cct gat ttt cgg gag aag gaa aca cct gag gac gaa tat ttt gaa gag	1488
118	Pro Asp Phe Pro Glu Lys Glu Thr Pro Glu Asp Glu Tyr Phe Ala Glu	
119	455	460
120	gaa tca atc aac agt tcc gga aac agc tat aat gaa atc cgt cgg cag	1536
121	Ala Ser Ile Asn Ser Ser Gly Asn Ser Tyr Thr Glu Ile Arg Ala Glu	
122	470	475
123	ctc cat aac cgt tcc gga tgg cgg gaa aag aaa aac gat caa tgg tat	1584
124	Leu Asn Asn Arg Ser Gly Trp Pro Ala Lys Lys Thr Asp Glu Leu Ser	
125	485	490
126	ctc cgt tac tcc gtt gac ttg acc gaa gct gta gaa gag gga tat tcc	1632
127	Phe Arg Tyr Tyr Val Asp Leu Thr Glu Ala Val Glu Ala Gly Tyr Ser	
128	500	505
129	gcc gaa gat ata aaa gtc aca gcc ggc tat aac gaa gag gct tgg gta	1680
130	Ala Glu Asp Ile Lys Val Thr Ala Gly Tyr Asn Glu Gly Ala Ser Val	
131	520	525
132	tca gag ctg aag cgg cat gac gct tca aag cgc att tac tat aca gaa	1728
133	Ser Glu Leu Lys Pro His Asp Ala Ser Lys His Ile Tyr Tyr Thr Glu	
134	535	540
135	gtc agc ttc acc ggg gtt ttg att tat cca ggc ggt caa tcc gcc cat	1776
136	Val Ser Phe Ser Gly Val Leu Ile Tyr Pro Gly Gly Gln Ser Ala His	
137	550	555
138	aaa aaa gaa gtg cag ttc cgc att tgg gca cca gac gga acc tat ttt	1824
139	Lys Lys Glu Val Gln Phe Arg Leu Ser Ala Pro Asp Gly Thr Ser Phe	
140	565	570
141	tgg aac cgg gaa aat gac cac tat tat cag ggt ctg tca cat cgc ctt	1872
142	Trp Asn Pro Glu Asn Asp His Ser Tyr Gln Gly Leu Ser His Ala Leu	

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142      585      585      590      595
144      ctc aag aag cgg tat att cct gtt tat gat gat gga cgg ctc gtt ttc      1920
146      Leu Lys Thr Arg Tyr Ile Pro Val Tyr Asp Asp Gly Arg Leu Val Phe
148      600      605      610
149      gga cat gag ccc ggt tac tag      1941
149      Gly His Glu Pro Gly Tyr
151      615
152 <210> 350 ID NO: 2
153 <211> LENGTH: 646
154 <212> TYPE: PRF
155 <213> ORGANISM: Bacillus licheniformis
156 <400> SEQUENCE: 2
157      Met Lys Ala Leu Cys Leu Ala Leu Leu Val Ile Phe Ser Met Ser Ile
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161      Ala Ser Phe Ser Glu Lys Thr Arg Ala Ala Ser Ala Glu Glu Tyr Pro
163      -10      -5      -1
165      His Asn Tyr Ala Glu Leu Leu Gln Lys Ser Leu Leu Phe Tyr Glu Ala
167      5      10      15
169      Glu Arg Ser Gly Arg Leu Pro Glu Asn Ser Arg Leu Asn Trp Arg Gly
171      20      25      30      35
173      Asp Ser Gly Leu Glu Asp Gly Lys Asp Val Gly Leu Asp Leu Thr Gly
175      40      45      50
177      Gly Trp Tyr Asp Ala Gly Asp His Val Lys Phe Gly Leu Pro Met Ala
179      55      60      65
181      Tyr Ser Ala Ala Ile Leu Ser Trp Ser Val Tyr Glu Tyr Arg Asp Ala
183      70      75      80
185      Tyr Lys Glu Ser Gly Gln Leu Asp Ala Ala Leu Asp Asn Ile Lys Trp
187      85      90      95
189      Ala Thr Asp Tyr Phe Leu Lys Ala His Thr Ala Pro Tyr Glu Leu Trp
191      100      105      110      115
193      Gly Gln Val Gly Asn Gly Ala Leu Asp His Ala Trp Trp Gly Pro Ala
195      120      125      130
197      Glu Val Met Pro Met Lys Arg Pro Ala Tyr Lys Ile Asp Ala Gly Cys
199      135      140      145
201      Pro Gly Ser Asp Leu Ala Gly Gly Thr Ala Ala Ala Leu Ala Ser Ala
203      150      155      160
205      Ser Ile Ile Phe Lys Pro Thr Asp Ser Ser Tyr Ser Glu Lys Leu Leu
207      165      170      175
209      Ala His Ala Lys Gln Leu Tyr Asp Phe Ala Asp Arg Tyr Arg Gly Lys
211      180      185      190      195
213      Tyr Ser Asp Cys Ile Thr Asp Ala Gln Gln Tyr Tyr Asn Ser Trp Ser
215      200      205      210
217      Gly Tyr Lys Asp Glu Leu Thr Trp Gly Ala Val Trp Leu Tyr Leu Ala
219      215      220      225
221      Thr Glu Glu Gln Gln Tyr Leu Asp Lys Ala Leu Ala Ser Val Ser Asp
223      230      235      240
225      Trp Gly Asp Pro Ala Asn Trp Pro Tyr Arg Trp Thr Leu Ser Trp Asp
227      245      250      255
229      Asp Val Thr Tyr Gly Ala Gln Leu Leu Leu Ala Arg Leu Thr Asn Asp

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193          265          270          275
194 Ser Arg Phe Val Lys Ser Val Glu Arg Asn Leu Asp Tyr Trp Ser Thr
195          280          285          290
196 Gly Tyr Ser His Arg Gly Ser Ile Glu Arg Ile Thr Tyr Thr Pro Gly
197          295          300          305
198 Gly Leu Ala Trp Leu Glu Gln Trp Gly Ser Leu Arg Tyr Ala Ser Asn
199          310          315          320
200 Ala Ala Phe Leu Ala Phe Val Tyr Ser Asp Trp Val Asp Thr Glu Lys
201          325          330          335
202 Ala Lys Arg Tyr Arg Asp Phe Ala Val Arg Gln Thr Glu Tyr Met Leu
203          340          345          350
204 Gly Asp Asn Pro Gln Gln Arg Ser Phe Val Val Gly Tyr Gly Lys Asn
205          355          360          365
206 Pro Pro Lys His Pro His His Arg Thr Ala His Gly Ser Trp Ala Asn
207          370          375          380
208 Gln Met Asn Val Pro Glu Asn His Arg His Thr Leu Tyr Gly Ala Leu
209          385          390          400
210 Val Gly Gly Pro Gly Arg Asp Asp Ser Tyr Arg Asp Asp Ile Thr Asp
211          405          410          415
212 Tyr Ala Ser Asn Glu Val Ala Ile Asp Tyr Asn Ala Ala Phe Thr Gly
213          420          425          430
214 Asn Val Ala Lys Met Phe Gln Leu Phe Gly Lys Gly His Val Pro Leu
215          435          440          445
216 Pro Asp Phe Pro Glu Lys Glu Thr Pro Glu Asp Glu Tyr Phe Ala Glu
217          450          455          460
218 Ala Ser Ile Asn Ser Ser Gly Asn Ser Tyr Thr Glu Ile Arg Ala Gln
219          465          470          475
220 Leu Asn Asn Arg Ser Gly Trp Pro Ala Lys Lys Thr Asp Gln Leu Ser
221          480          485          490
222 Phe Arg Tyr Tyr Val Asp Leu Thr Glu Ala Val Glu Ala Gly Tyr Ser
223          495          500          505
224 Ala Glu Asp Ile Lys Val Thr Ala Gly Tyr Asn Gln Gly Ala Ser Val
225          510          515          520
226 Ser Glu Leu Lys Pro His Asp Ala Ser Lys His Ile Tyr Tyr Thr Glu
227          525          530          535
228 Val Ser Phe Ser Gly Val Leu Ile Tyr Pro Gly Gly Gln Ser Ala His
229          540          545          550
230 Lys Lys Glu Val Gln Phe Arg Leu Ser Ala Pro Asp Gly Thr Ser Phe
231          555          560          565
232 Trp Asn Pro Glu Asn Asp His Ser Tyr Gln Gly Leu Ser His Ala Leu
233          570          575          580
234 Leu Lys Thr Arg Tyr Ile Pro Val Tyr Arg Asp Gly Arg Leu Val Phe
235          585          590          595
236 Gly His Glu Pro Gly Tyr
237          600          605          610
238          615
239 <210> SEQ ID NO: 3
240 <211> LENGTH: 42
241 <212> TYPE: DNA
242 <213> ORGANISM: Artificial Sequence

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**VERIFICATION SUMMARY**

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Input Set : N:\vernette\US09576778B.raw

Output Set: N:\CRF4\03122003\I576778B.raw

L:5 M:270 C: Current Application Number differs, Wrong Format  
L:6 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:22 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:0  
L:26 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:0  
L:26 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:0